RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: <u>69</u>

Source:

Date Processed by STIC:

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial	Number: 09/890, 836 CRF Edit Date: 8/29/6 Edited by: Z
	Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line
	Corrected the SEQ ID NO. Sequence numbers edited were:
<u>/</u>	Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
	Deleted: invalid beginning/end-of-file text; page numbers
• .	Inserted mandatory headings/numeric identifiers, specifically:
	Moved responses to same line as heading/numeric identifier, specifically:
_ 	Other:



IFW16

RAW SEQUENCE LISTING DATE: 08/29/2005 PATENT APPLICATION: US/09/890,836C TIME: 11:40:41

Input Set : A:\pto.kd.TXT

4 <110> APPLICANT: Andrew Bett

Output Set: N:\CRF4\08292005\1890836C.raw

```
5
              Volker Sandiq
              Rima Youil
      6
      8 <120> TITLE OF INVENTION: IMPROVED HELPER DEPENDENT VECTOR SYSTEM
              FOR GENE THERAPY
     11 <130> FILE REFERENCE: 20377YP
     13 <140> CURRENT APPLICATION NUMBER: US 09/890,836C
     14 <141> CURRENT FILING DATE: 2001-08-03
     16 <150> PRIOR APPLICATION NUMBER: PCT/US00/02405
     17 <151> PRIOR FILING DATE: 2000-01-31
     19 <150> PRIOR APPLICATION NUMBER: 60/138,134
     20 <151> PRIOR FILING DATE: 1999-06-08
     22 <150> PRIOR APPLICATION NUMBER: 60/118,601
     23 <151> PRIOR FILING DATE: 1999-02-04
     25 <160> NUMBER OF SEQ ID NOS: 17
     27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
     29 <210> SEQ ID NO: 1
     30 <211> LENGTH: 15
     31 <212> TYPE: DNA
     32 <213> ORGANISM: Artificial Sequence
     34 <220> FEATURE:
     35 <223> OTHER INFORMATION: Consensus sequence
W--> 37 <221> NAME/KEY: misc feature
     38 <222> LOCATION: (1)...(15)
     39 <223> OTHER INFORMATION: n = A, T, C or G
W--> 41 <400> 1
W--> 42 atttgnnnnn nnncg
                                                                            15
     44 <210> SEQ ID NO: 2
     45 <211> LENGTH: 10
     46 <212> TYPE: DNA
     47 <213> ORGANISM: Artificial Sequence
     49 <220> FEATURE:
     50 <223> OTHER INFORMATION: Adenovirus 5
     52 <400> SEQUENCE: 2
     53 attttgtgtt
                                                                                 10
     55 <210> SEO ID NO: 3
     56 <211> LENGTH: 10
     57 <212> TYPE: DNA
     58 <213> ORGANISM: Artificial Sequence
     60 <220> FEATURE:
     61 <223> OTHER INFORMATION: Consensus sequence
     63 <400> SEQUENCE: 3
     64 attttgttgt
                                                                                 10
```

Input Set : A:\pto.kd.TXT

Output Set: N:\CRF4\08292005\1890836C.raw

66 <210> SEQ ID NO: 4 67 <211> LENGTH: 158 68 <212> TYPE: DNA	
69 <213> ORGANISM: Artificial Sequence	
71 <220> FEATURE:	
72 <223> OTHER INFORMATION: Synthetic packaging signal 74 <400> SEQUENCE: 4	
75 gtacacagga agtgactttt aacgcgcggt ttgttacgga tgttgtagta aatttgtcta	60
76 gggccgagta agatttgacc gtttacgcgg ggactttgaa taagagcgag tgaaatctga	120
77 ataattttgt tgtactcata gcgcgtaatc tctagacg	158
79 <210> SEQ ID NO: 5	
80 <211> LENGTH: 158	
81 <212> TYPE: DNA 82 <213> ORGANISM: Artificial Sequence	
84 <220> FEATURE:	
85 <223> OTHER INFORMATION: Adenovirus 5	
87 <400> SEQUENCE: 5	
88 gtacacagga agtgacaatt ttcgcgcggt tttaggcgga tgttgtagta aatttgggcg	60
89 taaccgagta agatttggcc attttcgcgg gaaaactgaa taagaggaag tgaaatctga	120
90 ataattttgt gttactcata gcgcgtaatc tctagacg	158
92 <210> SEQ ID NO: 6 93 <211> LENGTH: 65	
94 <212> TYPE: DNA	
95 <213> ORGANISM: Artificial Sequence	
97 <220> FEATURE:	
98 <223> OTHER INFORMATION: Linker	
100 <400> SEQUENCE: 6	
101 agctcggccg attattggcg cgccagatct gcggccgctt ctagaaacgc gtgaattcgg	60
102 cgcca 105 <210> SEQ ID NO: 7	65
105 <210> SEQ 1D NO: 7	
107 <212> TYPE: DNA	
108 <213> ORGANISM: Artificial Sequence	
110 <220> FEATURE:	
111 <223> OTHER INFORMATION: Linker	
113 <400> SEQUENCE: 7	60
114 agettggege egaatteaeg egtttetaga ageggeegea gatetggege gecaataate	60 65
115 ggccg 118 <210> SEQ ID NO: 8	0.5
119 <211> LENGTH: 40	
120 <212> TYPE: DNA	
121 <213> ORGANISM: Artificial Sequence	
123 <220> FEATURE:	
124 <223> OTHER INFORMATION: PCR Primer	
126 <400> SEQUENCE: 8 127 attggcgcgc cttctttctg ggatgattca gcatcaactc	40
127 attggegege ettetttetg ggatgattea geateaaete 129 <210> SEQ ID NO: 9	40
130 <211> LENGTH: 41	
131 <212> TYPE: DNA	

Input Set : A:\pto.kd.TXT

Output Set: N:\CRF4\08292005\I890836C.raw

132 <213> ORGANISM: Artificial Sequence 134 <220> FEATURE: 135 <223> OTHER INFORMATION: PCR Primer 137 <400> SEQUENCE: 9 41 138 gatcgtcggc cgcttgggtc atagacttct ttgagaacca g 140 <210> SEO ID NO: 10 141 <211> LENGTH: 41 142 <212> TYPE: DNA 143 <213> ORGANISM: Artificial Sequence 145 <220> FEATURE: 146 <223> OTHER INFORMATION: PCR Primer 148 <400> SEQUENCE: 10 149 atcagttagc ggccgcacaa gctaagatca caaagctgtt t 41 151 <210> SEQ ID NO: 11 152 <211> LENGTH: 37 153 <212> TYPE: DNA 154 <213> ORGANISM: Artificial Sequence 156 <220> FEATURE: 157 <223> OTHER INFORMATION: PCR Primer 159 <400> SEQUENCE: 11 37 160 tatggcgcgc cgctgacacc cagcctgggt gccggtg 162 <210> SEQ ID NO: 12 163 <211> LENGTH: 39 164 <212> TYPE: DNA 165 <213> ORGANISM: Artificial Sequence 167 <220> FEATURE: 168 <223> OTHER INFORMATION: PCR Primer 170 <400> SEQUENCE: 12 39 171 tcgacgcgta gcgctgtgtg gccttggcag tttccatag 173 <210> SEQ ID NO: 13 174 <211> LENGTH: 45 175 <212> TYPE: DNA 176 <213> ORGANISM: Artificial Sequence 178 <220> FEATURE: 179 <223> OTHER INFORMATION: PCR Primer 181 <400> SEQUENCE: 13 45 182 tcagtaatgc ggccgcggga tcattcctgg actcagattg ttctg 184 <210> SEQ ID NO: 14 185 <211> LENGTH: 41 186 <212> TYPE: DNA 187 <213> ORGANISM: Artificial Sequence 189 <220> FEATURE: 190 <223> OTHER INFORMATION: PCR Primer 192 <400> SEQUENCE: 14 41 193 tattaaggcg ccgggcatgg gagtgatctc accaactctg g 195 <210> SEQ ID NO: 15 196 <211> LENGTH: 46 197 <212> TYPE: DNA 198 <213> ORGANISM: Artificial Sequence

Input Set : A:\pto.kd.TXT

Output Set: N:\CRF4\08292005\I890836C.raw

200	<220> FEATUR	E:					
201	<223> OTHER INFORMATION: PCR Primer						
203	3 <400> SEQUENCE: 15						
204	tcgacgcgta t	ttaaatgtg	ctggagtgtt	gagatactgt	agtggt		46
	<210> SEQ ID						
207	<211> LENGTH	: 28068					
	<212> TYPE: 3						
209	<213> ORGANI	SM: Artifi	cial Sequer	nce			
	<220> FEATUR		_				
212	<223> OTHER	INFORMATIO	N: Modified	d adenovirus	3		
214	<400> SEQUEN	CE: 16					
215	aaacatcatc a	ataatatac	cttattttgg	attgaagcca	atatgataat	gagggggtgg	60
	agtttgtgac g						120
	tgtgatgttg c						180
	ttggtgtgcg c						240
	tagtaaattt g			_			300
	ggaagtgaaa t						360
	ggggactttg a				-		420
	ttccgggtca a						480
	agttataagc t				-		540
	cccaccaaca t						600
	ggatctcatg t						660
	aagctaagtc a						720
	ccccacccca c						780
	aggtatgtgt g						840
	aacagtcacg a						900
230	accccactag g	gccccaaga	ttttaggact	tgtgtgtggg	tgggacctcc	cctttctatc	960
	atgctttaga a						1020
232	ttcagccaaa g	gcaattaaa	ataacttcat	acttgatatc	catgtcagca	aaagctgcaa	1080
233	aacgcaaatg g	gtggctgct	aagagccctg	gtaccctgac	gagcacacca	agtgcttagc	1140
234	aacagtggtg t	ccaaaggac	cagctggaag	cctgccttga	tgagaagttg	ctcttcttc	1200
235	tacatgaagg a	acacctcta	ctctcctgct	tttaatacct	gagctgtgag	tgatcatcta	1260
236	tgtccattag c	aaacatccc	agtggagaag	gaaacactca	tacccgaaat	ctaagctaca	1320
237	tagttggaat c	acttcaact	tattgcaata	aacacttact	aagcacctat	tgtgggcaag	1380
238	tctttgcaat g	gataatagt	tcagtagata	ttttgatgta	atatttgaaa	taacaataaa	1440
239	aattgccacc a	ctgaattta	ttgagcattt	gctgtgcttt	aggcactaac	ccaggttctt	1500
240	taaatatttg g	tcttattcg	atctgtataa	atagccatct	atgagaaagg	gactattatt	1560
241	gcccttattt t	acaaatgag	gccaatgagg	·cccagagagg	ttaactaagt	tgcccaaaat	1620
242	catacagccc a	ctagtggca	gagcaggatg	caaacccagg	cttgcctcgt	tcccaagccc	1680
	acatgtcgtt t						1740
244	taagcaagtt t	tgaaacata	gaaacttaaa	atgtgccatt	aagaaaagta	caggcaaggt	1800
245	tttccaaggg g	aggtgtgga	cctccggaca	aatttttaag	aactaattat	aaatacttaa	1860
	aaatgggaat a						1920
	cctctaaaac c		_	_	-		1980
	tttctatgta c						2040
249	gagggctcag te	gcccctccc	atggggtggt	tagtgagtac	agagctgagc	tcaccggcca	2100
	tetgeagett ca						2160
	agcagaggca t						2220
252	taactttaaa ta	accatttta	tagccacact	ggagttttga	agacctcaat	atgcaaatat	2280

Input Set : A:\pto.kd.TXT

Output Set: N:\CRF4\08292005\I890836C.raw

253	tactcaggtt	ctgattactt	gtctgctcca	tgataacaca	ctctaaaagc	aatgaatggg	2340
254	gcttatttgt	agagaactga	agcattttaa	gcttttgctc	aggaatccct	ggtagcttcc	2400
				agaaacagga			2460
256	cgcagtgcct	cagtagtcca	tcaggcagaa	aaaactgcag	atggcacatg	gaaatgacca	2520
257	gcggcggaag	ataccccgac	agtgtgggca	gttctatttc	agcagcaatc	aagaggggc	2580
258	ctggagccac	tcaatcaagt	ggagcaggat	gggagcaagc	actgtgcaga	ccaatgcaat	2640
				gatgagattc			2700
				tttctccatt			2760
				caacctccac			2820
				gtaaatccat			2880
				ttggtgggca			2940
				gaagtaagcc			3000
				ttactcatcc			3060
				tcagcccagt			3120
				caagtgcaag			3180
				ccccagtcat			3240
				ctgtgcttgt			3300
				gggaattctg			3360
				ccaggtccag			3420
				tcttaatcat			3480
				agcaaatact			3540
		-		ggcacttggg			3600
				caatgataaa			3660
				ggtgggttta			3720
				acatcagcta			3780
				atgtgaattt			3840
				tcaagtcaca			3900
				cctgggtttg			3960
				ctccttctct			4020
				ttctgtagct			4080
				ttcagctgct			4140
				gatattggcc			4200
				tatagtagtg			4260
				attctggaat			4320
				tgtaacagaa			4380
				aaagatgctc			4440
				gttcaagtca			4500
				gaggtgaagg			4560
				gccccatatc			4620
				gaaacaggaa			4680
				tggccaagtg			4740
				agaaagctgt			4800
				catccaacag			4860
	_			tgcaggatct			4920
				cttacggcag			4980
		-		tggcaaaagg			5040
	-			gcagatggag			5100
				aaacagttgt			5160
				aatggcaaat			5220

Input Set : A:\pto.kd.TXT

Output Set: N:\CRF4\08292005\1890836C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 6,7,8,9,10,11,12,13

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:6; Line(s) 102
Seq#:7; Line(s) 115

VERIFICATION SUMMARY

DATE: 08/29/2005

PATENT APPLICATION: US/09/890,836C

TIME: 11:40:42

Input Set : A:\pto.kd.TXT

Output Set: N:\CRF4\08292005\1890836C.raw

L:37 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:41 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1

L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

Raw Sequence Listing before editing, for reference only



IFW16

RAW SEQUENCE LISTING

DATE: 08/20/2005

PATENT APPLICATION: US/09/890,836C

TIME: 11:46:20

Does Not Comply

Input Set : A:\pto.da.TXT

Output Set: N:\CRF4\08202005\1890836C.raw

- 4 <110> APPLICANT: Andrew Bett
- Volker Sandiq
- Rima Youil
- 8 <120> TITLE OF INVENTION: IMPROVED HELPER DEPENDENT VECTOR SYSTEM
- FOR GENE THERAPY
- 11 <130> FILE REFERENCE: 20377YP
- 13 <140> CURRENT APPLICATION NUMBER: US 09/890,836C
- 14 <141> CURRENT FILING DATE: 2001-08-03
- 16 <150> PRIOR APPLICATION NUMBER: PCT/US00/02405
- 17 <151> PRIOR FILING DATE: 2000-01-31
- 19 <150> PRIOR APPLICATION NUMBER: 60/138,134
- 20 <151> PRIOR FILING DATE: 1999-06-08
- 22 <150> PRIOR APPLICATION NUMBER: 60/118,601
- 23 <151> PRIOR FILING DATE: 1999-02-04
- 25 <160> NUMBER OF SEQ ID NOS: 17
- 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ERRORED SEQUENCES

- 66 <210> SEO ID NO: 4
- 67 <211> LENGTH: 158
- 68 <212> TYPE: DNA
- 69 <213> ORGANISM: Artificial Sequence
- 71 <220> FEATURE:
- 72 <223> OTHER INFORMATION: Synthetic packaging signal
- 74 <400> SEQUENCE: 4
- E--> 75 gtacacagga agtgactttt aacgcgcggt ttgttacgga tgttgtagta aatttgtcta
- W--> 76(60)gggccgagta agatttgacc gtttacgcgg ggactttgaa taagagcgag tgaaatctga
- E--> 77 (120) ataattttgt tgtactcata gcgcgtaatc tctagacg
 - 79 <210> SEQ ID NO: 5
 - 80 <211> LENGTH: 158
 - 81 <212> TYPE: DNA
 - 82 <213> ORGANISM: Artificial Sequence
 - 84 <220> FEATURE:
 - 85 <223> OTHER INFORMATION: Adenovirus 5
 - 87 <400> SEQUENCE: 5
- E--> 88 gtacacagga agtgacaatt ttcgcgcggt tttaggcgga tgttgtagta aatttgggcg
- W--> 89 60taaccgagta agatttggcc attttcgcgg gaaaactgaa taagaggaag tgaaatctga
- E--> 90 120ataattttgt gttactcata gcgcgtaatc tctagacg
 - 92 <210> SEQ ID NO: 6
 - 93 <211> LENGTH: 65
 - 94 <212> TYPE: DNA

Corrected Diskette Needed

158 \

¢ćġcca

6pggccg

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/890,836C

DATE: 08/20/2005 TIME: 11:46:20

Input Set : A:\pto.da.TXT

Output Set: N:\CRF4\08202005\I890836C.raw

95 <213> ORGANISM: Artificial Sequence

97 <220> FEATURE:

98 <223> OTHER INFORMATION: Linker

100 <400> SEQUENCE: 6

W--> 101 agctcggccg attattggcg cgccagatct gcggccgctt ctagaaacgc gtgaattcgg

E--> 102 65

104 <210> SEQ ID NO: 7

105 <211> LENGTH: 65

106 <212> TYPE: DNA

107 <213> ORGANISM: Artificial Sequence

109 <220> FEATURE:

110 <223> OTHER INFORMATION: Linker

112 <400> SEQUENCE: 7

W--> 113 agettggege egaatteaeg egtttetaga ageggeegea gatetggege gecaataate

E--> 114 65

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/890,836C

DATE: 08/20/2005 TIME: 11:46:21

Input Set : A:\pto.da.TXT

Optput Set: N:\CRF4\08202005\1890836C.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:6; Line(s) 101
Seq#:7; Line(s) 113

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/890,836C

DATE: 08/20/2005 TIME: 11:46:21

Input Set : A:\pto.da.TXT

L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7

L:114 M:252 E: No. of Seq. differs, <211> LENGTH:Input:65 Found:0 SEQ:7

L:114 M:301 E: (44) No Sequence Data was Shown, SEQ ID:7

Output Set: N:\CRF4\08202005\1890836C.raw

L:37 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:41 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1 L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0 _L:75 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:4 L:76 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6 L:77 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4 M:254 Repeated in SeqNo=4 L:77 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3 L:77 M:252 E: No. of Seq. differs, <211> LENGTH:Input:158 Found:98 SEQ:4 L:88 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:5 L:89 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6 L:90 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5 M:254 Repeated in SeqNo=5 L:90 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3 L:90 M:252 E: No. of Seq. differs, <211> LENGTH:Input:158 Found:98 SEQ:5 L:101 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7 L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:102 M:301 E: (44) No Sequence Data was Shown, SEQ ID:6 - L:102 M:252 E: No. of Seq. differs, <211> LENGTH:Input:65 Found:0 SEQ:6 L:113 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7